

FIG. 1

Sequence of human APRIL (SEQ ID NOS: 1 and 2)

Human G70 cDNA (SEQ ID NO 1)

Length: 1465 bp

```
1  GCCAACCTTC CCTCCCCAA CCCTGGGGCC GCCCCAGGGT TCCTGCGCAC
51  TGCCTGTTCC TCCTGGGTGT CACTGGCAGC CCTGTCTTTC CTAGAGGGAC
101  TGAACCTAA TTCTCCTGAG GCTGAGGGAG GGTGGAGGGT CTCAAGGCCAA
151  CGCTGGCCCC ACGACGGAGT GCCAGGAGCA CTAACAGTAC CCTTAGCTTG
201  CTTTCCTCCT CCCTCCTTTT TATTTTCAAG TTCCTTTTAA TTTCTCCTTG
251  CGTAACAACC TTCTTCCCTT CTGCACCACT GCCCGTACCC TTACCCGCCCC
301  CGCCACCTCC TTGCTACCCC ACTCTTGAAA CCACAGCTGT TGGCAGGGTC
351  CCCAGCTCAT GCCAGCCTCA TCTCCTTTCT TGCTAGCCCC CAAAGGGCCT
401  CCAGGCAACA TGGGGGGCCC AGTCAGAGAG CCGGCACCTC CAGTTGCCCT
451  CTGGTTGAGT TGGGGGGCAG CTCTGGGGGC CGTGGCTTGT GCCATGGCTC
501  TGCTGACCCA ACAAAACAGAG CTGCAGAGCC TCAGGAGAGA GGTGAGCCGG
551  CTGCAGGGGA CAGGAGGCCC CTCCCAGAAT GGGGAAGGGT ATCCCTGGCA
601  GAGTCTCCCG GAGCAGAGTT CCGATGCCCT GGAAGCCTGG GAGAGTGGGG
651  AGAGATCCCC GAAAAGGAGA GCAGTGCTCA CCCAAAAACA GAAGAAGCAG
701  CACTCTGTCC TGCACCTGGT TCCCATTAA CACCCTCCA AGGATGACTC
751  CGATGTGACA GAGGTGATGT GGCAACCAGC TCTTAGCGCT GGGAGAGGCC
801  TACAGGCCCA AGGATATGGT GTCCGAATCC AGGATGCTGG AGTTTATCTG
851  CTGTATAGCC AGGTCTCTGT TCAAGACGTG ACTTTCACCA TGGGTCAAGT
901  GGTGTCTCGA GAAGGCCAAG GAAGGCAGGA GACTCTATTC CGATGTATAA
951  GAAGTATGCC CTCCCACCCG GACCGGGCCT ACAACAGCTG CTATAGCGCA
1001 GGTGTCTTCC ATTTACACCA AGGGGATATT CTGAGTGTC AATTTCCCCG
1051 GGCAAGGGCG AAACCTAACC TCTCTCCACA TGGAACCTTC CTGGGGTTTG
1101 TGAACTGTG ATTGTGTTAT AAAAAGTGCC TCCCAGCTTG GAAGACCAGG
1151 GTGGGTACAT ACTGGAGACA GCCAAGAGCT GAGTATATAA AGGAGAGGGA
1201 ATGTGCAGGA ACAGAGGCGT CTCCTGGGT TTGGCTCCCC GTTCCTCACT
1251 TTTCCCTTTT CATTCCCACC CCCTAGACTT TGATTTTACG GATATCTTGC
1301 TTCTGTTCCT CATGGAGCTC CGAATCTTGG CGTGTGTGTA GATGAGGGGC
1351 GGGGGACGGG GCCAGGCAT TGTTACAGAC TGCTCGGGGC CCACTGGAAG
1401 CATCCAGAAC AGCACCACCA TCTAACGGCC GCTCGAGGGA AGCACCCTGC
1451 GGTTTGGGGC AAGTC
```

The proposed transmembrane domains are boxed

human G70 protein sequence (SEQ ID NO 2)

```
1  MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT
51  QQTELQSLRR EVSRLQGTGG PSQNEGEPYV QSLPEQSSDA LEAWESGERS
101  RKRRAVLTQK QKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA
151  QGYGVRIQDA GYVLLYSQVL FQDVTFTMGQ VVSREGQGRQ ETLFRCIKRM
201  PSHPDRAVNS CYSAGVFHLH QGDILSVIIP RARAKLNLSP HGTFLGFV
```

FIG. 2A

Sequence of mouse G70 (SEQ ID NOS: 3 and 4)

Mouse G70 (SEQ ID NO 3)

1	CATGCCGAGT	GCTTGTGTGTG	TGTTACCTGC	TCTAAGAAGC	TGGCTGGGCA
51	GCGTTTCACC	GCTGTGGAGG	ACCACTATTA	CTGCGTGGAT	TGCTACAAGA
101	ACTTTGTGGC	CAAGAAGTGT	GCTGGATGCA	AGAACCCCAT	CACTGGGTTT
151	GGTAAAGGCT	CCAGTGTGGT	GGCCTATGAA	GGACAATCCT	GGCAGCACTA
201	CTGCTTCCAC	TGCAAAAAAT	GCTCCGTGAA	TCTGGCCAAC	AAGCGCTTTG
251	TATTTCTATA	TGAGCAGGTG	TATTGCCCTG	ACTGTGCCAA	AAAGCTGTAA
301	CTTGACGGCT	GCCCTGTCTT	TCCTAGATAA	TGGCACCAAA	TTCTCCTGAG
351	GCTAGGGGGG	AAGGAGTGTC	AGAGTGTCAC	TAGCTCGACC	CTGGGGACAA
401	GGGGGACTAA	TAGTACCCTA	GCTTGATTTC	TTCCCTATTCT	CAAGTTCCCTT
451	TTTATTTCTC	CCTTGCGTAA	CCCGCTCTTC	CCTTCTGTGC	CTTTGCCTGT
501	ATTTCCACCC	TCCCTGCTAC	CTCTTGGCCA	CCTCACTTTCT	GAGACCACAG
551	CTGTTGGCAG	GGTCCCTAGC	TCATGCCAGC	CTCATCTCCA	GGCCACATGG
601	GGGGCTCAGT	CAGAGAGCCA	GCCCTTTTCG	TTGCTCTTTG	GTTGAGTTGG
651	GGGGCAGTTC	TGGGGGCTGT	GACTTGTGCT	GTCGCACTAC	TGATCCAACA
701	GACAGAGCTG	CAAAGCCTAA	GGCGGGAGGT	GAGCCGGCTG	CAGCGGAGTG
751	GAGGGCCTTC	CCAGAAGCAG	GGAGAGCGCC	CATGGCAGAG	CCTCTGGGAG
801	CAGAGTCTCT	ATGTCCTGGA	AGCCTGGAAG	GATGGGGCGA	AATCTCGGAG
851	AAGGAGAGCA	GTA CTACCC	AGAAGCACAA	GAAGAAGCAC	TCAGTCCTGC
901	ATCTTGTCTC	AGTTAACATT	ACCTCCAAGG	ACTCTGACGT	GACAGAGGTG
951	ATGTGGCAAC	CAGTACTTAG	GCGTGGGAGA	GGCCTGGAGG	CCCAGGGAGA
1001	CATTGTACGA	GCTCGGGACA	CTGGAATTTA	TCTGCTCTAT	AGTCAGGTCC
1051	TGTTTCATGA	TGTGACTTTC	ACAATGGGTC	AGGTGGTATC	TCGGGAAGGA
1101	CAAGGGAGAA	GAGAACTCT	ATTCCGATGT	ATCAGAAGTA	TGCCTTCTGA
1151	TCCTGACCGT	GCCTACAATA	GCTGCTACAG	TGCAGGTGTC	TTTCATTTTC
1201	ATCAAGGGGA	TATTATCACT	GTCAAAATTC	CACGGGCAAA	CGCAAAACTT
1251	AGCCTTTCTC	CGCATGGAAC	ATTCTGGGGG	TTTGTGAAAC	TATGATTGTT
1301	ATAAAGGGGG	TGGGGATTTC	CCATTCCAAA	AACTGGCTAG	ACAAAGGACA
1351	AGGAACGGTC	AAGAACAGCT	CTCCATGGCT	TTGCCTTGAC	TGTTGTCTCT
1401	CCCTTTGCCT	TTCCCGCTCC	CACATATCTG	GCTTTTGACTC	CATGGATATT
1451	AAAAAAGTAG	AATATTTTGT	GTTTATCTCC	CAAAAA	

FIG. 2B

Mouse G70 Length: 241 (SEQ ID NO 4)

1 MPASSPGHMG GSVREPALSV ALWLSWGA VL GAVTCAVALL IQQTELQSLR
51 REVSRLQRSG GPSQKQGERP WQSLWEQSPD VLEAWKDGA K SRRRRAVLTQ
101 KHKKKH SVLH LVPVNITSKD SDVTEVMWQP VLRRGRGLEA QGDIVRVWDT
151 GIYLLYSQVL FHDVTF TMGQ VVSREGQGRR ETLFRCIRSM PSDPDRA YNS
201 CYSAGVFHLH QGDIITVKIP RANAKLSLSP HGTFLGFVKL *

G-70 FLAG des92 (smuG70) Strain #4081 (SEQ ID NO 19):

MDYKDDDDKKHKKH SVLHLVPVNITSKDS DVTEVMWQPV LRRGRGLEA QGDIVRVWDTGIY
LLYSQVL FHDVTF TMGQVVSREGQGRR ETLFRCIRSMPSDPDRAYNSCYSAGVFHLH QGDII
TVKIPRANAKLSLSP HGTFLGFVKL*

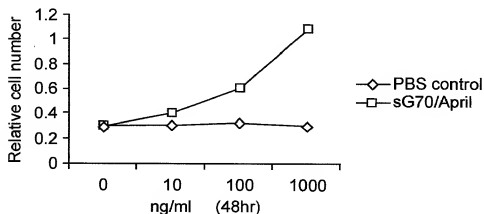
FIG. 3

Alignm. of human and mouse G70

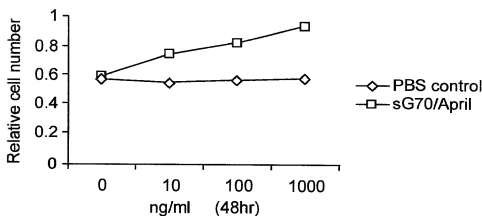
mouse:	1	MPASS-----PGHMGGS	VREPALSVALWLSGAVLGAVTCAVALI	IQTELOSLRR	51
		MPASS	PG+MG	VREPALSVALWLSGA LGAV CA+ALL	QQTELOSLRR
human:	1	MPASSPFLAPKGP	GNMG	GFPVREPALSVALWLSGAAAGAVACAWALL	IQTELOSLRR
mouse:	52	EVSLQRSGPSQ	KQGERPWQSLWEQSPD	VLEAWKDGAKSRRRRAVL	TQKHKKHSHVLHL
		EVSLQ	+GGFSQ	PWQSL EQS D LEAW+ G +SR+RRAVLTQK	KK+HSHVLHL
human:	61	EVSLQGTG	GPSNGEGYFWQSLPEQSSDALEAMESGERSKRRRAVL	TQKQKQHSHVLHL	120
mouse:	112	VPVNITSD	-SDVTEVMWPV	LRRGRLG	EAQGDIVRVWDTGIYLLYSQVLFHDVDTFMGQ
		VP+N	TSKD	SDVTEVMWP	LRRGRL+AQG VR+ D G+YLLYSQVLE DVDTFMGQ
human:	121	VPINATSKD	SDVTEVMWP	ALRRGRLG	LQAQGYGVRIDAGVYLLYSQVLFQDVDTFMGQ
mouse:	171	VVSREGQGR	ETLFR	CIRSMPSD	PDRAVNSCYSAGVFHLHQGDIIIVKIPRANAKLSLP
		VVSREGQGR	+ETLFR	CIRSMPS	PDRAVNSCYSAGVFHLHQGDI+V IPRA AKL+LSP
human:	181	VVSREGQGR	QETLFR	CIRSMPSH	PDRAVNSCYSAGVFHLHQGDILSVIIPRANAKLNSP
mouse:	231	HGTF	LG	VFVKL	240
		HGTF	LG	VFVKL	
human:	241	HGTF	LG	VFVKL	250

FIG. 4A

Effect of sG70/April on Raji cell proliferation



Effect of sG70/April on Jurkat cell proliferation



Effect of sG70/April on K562 cell proliferation

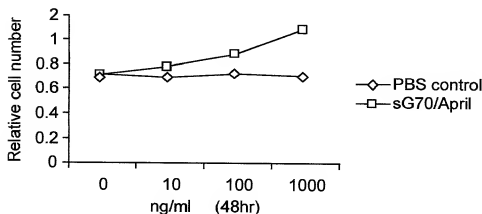
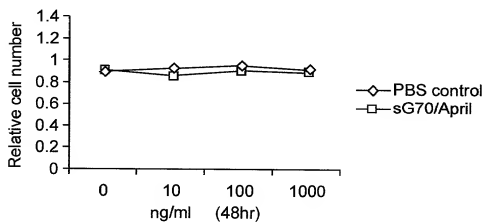
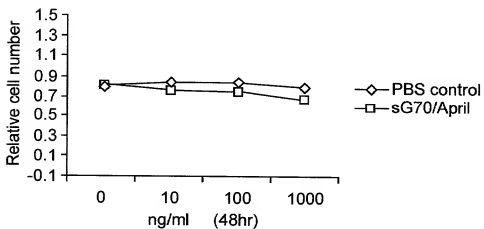


FIG. 4B

Effect of sG70/April on U937 cell proliferation



Effect of sG70/April on 293 T cell proliferation



Effect of sG70/April on 3T3 cell proliferation

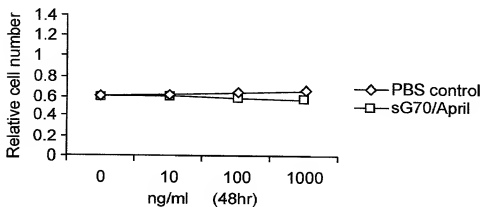


FIG. 5A

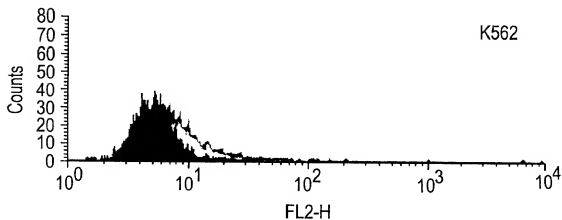
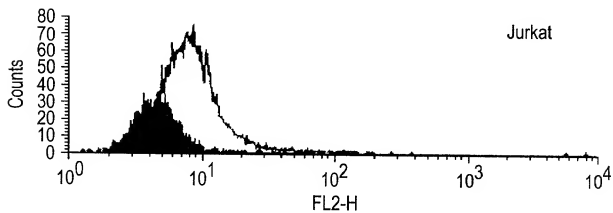
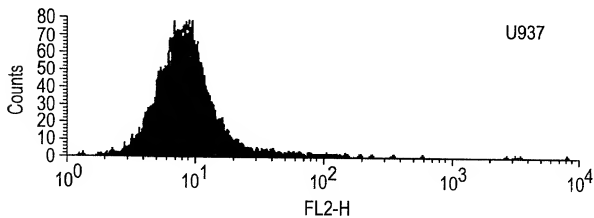


FIG. 5B-1

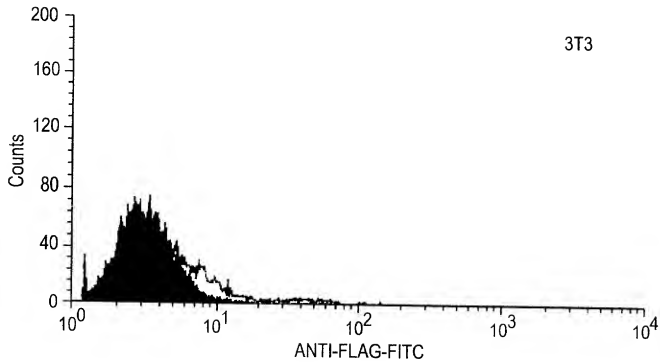


FIG. 5B-2

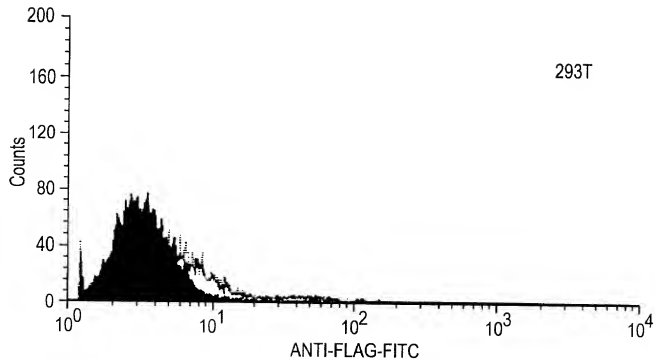


FIG. 5B-3

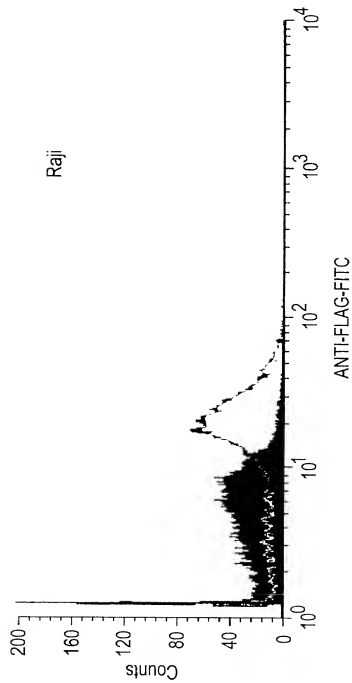
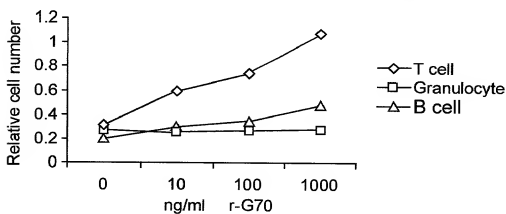


FIG. 6

The effect of r-G70/April on human
peripheral blood B cell, T cell and Granulocyte



The effect of IL-2 and G70/April on human
peripheral T cell proliferation

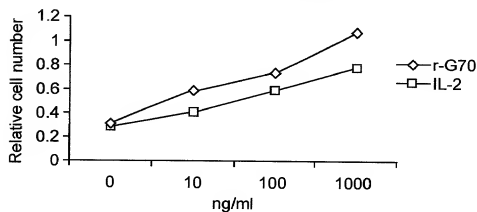
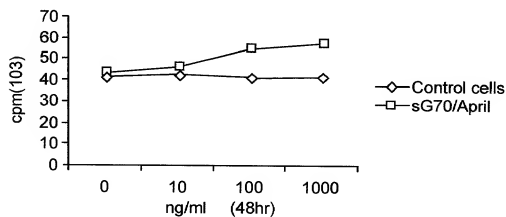


FIG. 7

Effect of sG70/April on murine B cell
proliferation



Effect of sG70/April on murine T cell
proliferation

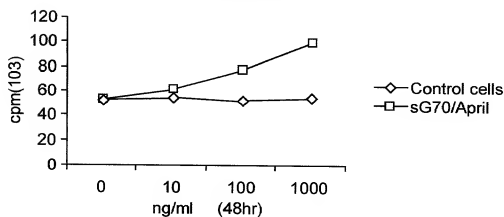


FIG. 8

Effect of G70/April on murine T cell
proliferation costimulated through CD28
antibody

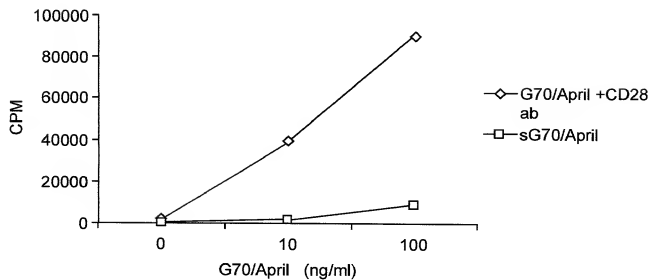


FIG. 9

Co-stimulatory activity of G70/April on mouse T cells

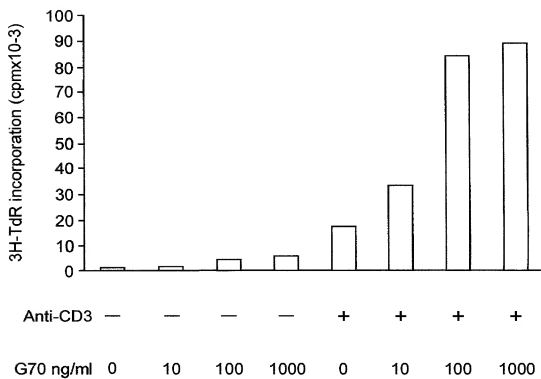


FIG. 10A

Human BCMA

Human (SEQ ID NO: 5):

1 MAGQCSQNEY FDSLHACIP CQLRCSSNTP PLTCQRYCNA SVTNSVKGTN
51 AILWTCLGLS LIISLAVFVL MFLLRKISSE PLKDEFKNTG SGLLGMANID
101 LEKSRTGDEI ILPRGLEYTV EECTCEDCIK SKPKVSDHC FLPAMEEGA
151 TILVTTKTND YCKSLPAALS ATEIEKSISA R

Human (SEQ ID NO: 5):

MAGQ**CSQ** NEY**FDSL**LLHA CIP**CQLRCSS** NTP**PLTCQRY** CNASVTNSVK
GTNA ILWTCL GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA
NIDLEKSRTG DEIILPRGLE YTVEECTCED CIKSKPKVDS DHCFLPAME
EGATILVTTK TNDYCKSLPA ALSATEIEKS ISAR

hBCMA's extracellular domain (SEQ ID NO: 6):

MAGQCSQ NEYFDSL**LLHA** CIP**CQLRCSS** NTP**PLTCQRY** CNASVTNSVK
GTNA

hBCMA's cysteine-rich consensus region (SEQ ID NO: 7):

CSQ NEYFDSL**LLHA** CIP**CQLRCSS** NTP**PLTCQRY** C

hBCMA's transmembrane region (SEQ ID NO: 8):

ILWTCL GLSLIISLAV FVLMF

FIG. 10B

huBCMA-Fc (SEQ ID NO: 9):

MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAGGG
GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
LSLSPGK*

muBCMA-Fc (SEQ ID NO: 10):

MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGSYTGGGGG
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK*

FIG. 11

FIG. 11

Alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence

murine BCMA amino acid sequence Length: 185 (SEQ ID NO: 11):

1 MAQOCFSEY FDSLHACKP CHLRCSNPPA TCQPYCDPSV TSSVKGFTV
51 LWFILGLTIV LSLALFTISF LLRNMPEAL KDEPQSPQL DGSQLODKAD
101 TELTRIRAGD DRIFPRSLEY TVEECTCEDC VKSKPKGDS D HFFPLPAMEE
151 GATILVTTKT GDYKSSVPT ALQSVGMGEK PTHTR

alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence.

Query: 4 MAGOCQNEVYDLSLLHACIPQLRCSNTPPLTCQRYCNASVTSVKGFTVAILWTCLGLS 63
MA QC +EYFDSLHAC PC LRCS+ PP TCQ YC+ SVT+SVKGT +LW IGL+
Sbjct: 1 MAQOCFSEYFDSLHACKPCHLRCSN--PPATCQPYCDEFSVTSSVKGFTVILWIFLGLT 58
Query: 64 LIISIAVFLVILFKISSBFLKDEFKNTG----SGLLGMANIDLEKSRGTGDEILPRGL 119
L++SLA+F + FLIRK++ E LKDE ++ G S L A+ +L + R GD+ I PR L
Sbjct: 59 LVLSIALFTTISFLRKWNPEALKDEPQSGQLDGSQLODKADTELTRIRAGDRIFFRSL 118
Query: 120 EYTVECTCEDCIKSKPKVDSHDHCFPLPAMEEGATILVTTKTDYCKS-LPAAL-SATEI 177
EYTVECTCEDC+KSKPK DSDH FPLPAMEEGATILVTTKT DY KS +P AL S +
Sbjct: 119 EYTVECTCEDCVKSKPKGDSHFFPLPAMEEGATILVTTKTDYKSSVPTALQSVGMG 178
Query: 178 EKSIAR 184
EK R
Sbjct: 179 EKPTHTR 185

FIG. 12A

Human TACI

huTACI (SEQ ID NO: 14).

1 MSLGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSL S CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR
201 PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT
251 PDPTCAGR WG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

MSLGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC
KTICNHQSQRTCAAFCRSL**SCRKEQGKFYD**HLLRDCISCASICGQHPKQC
AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPAL
PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR
PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAPTQESAVTPGT
PDPTCAGR WGC HTRTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

huTACI's extracellular domain (SEQ ID NO: 15):

1 MSLGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSL S CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYST

FIG. 12B

huTACI's cysteine-rich consensus region (SEQ ID NO: 16):

CPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFc and
CRKEQGKFYDHLLRDCISCASICGQHPKQCAYFC

transmembrane region (SEQ ID NO: 17):

LGLCLCAVLCCFLVAVACFL

hTACI-Fc (SEQ ID NO: 18):

1 MSGLGSRRRG GRSRVDQEEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCSRSLs CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYSGGGGG DKHTTCP PCP APELLGGPSV FLFPKPKDT
201 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
251 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
301 LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
351 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK*

FIG. 13

Alignment of cysteine rich extracellular regions of human TACI and human BCMA.

```
34 CP EEQYWDPLLGT C MSCKTICNHQS.QRTCAAFCRSLSCRKEQGKFYDHL 82
   | : :|. | || |. |. |. . || :| . . | . :
8 CSQNEYFDSL LHACIPQLRCSSNTPLP LTCQRYCNASVTNSVKGT..NAI 55

      .
83 LRDCISCASI 92
   | | : . |
56 LWTCLGLSLI 65
```

FIG. 14A

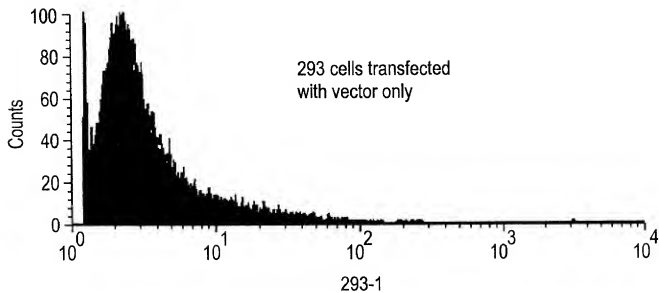


FIG. 14B

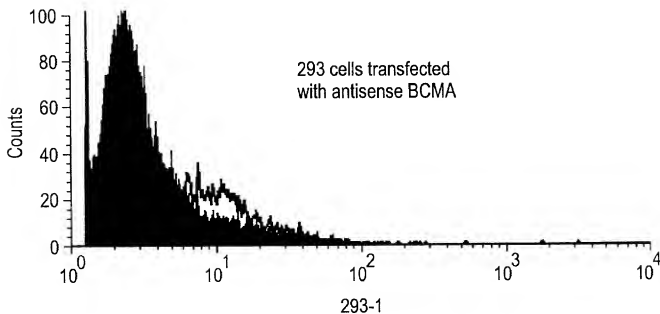


FIG. 14C

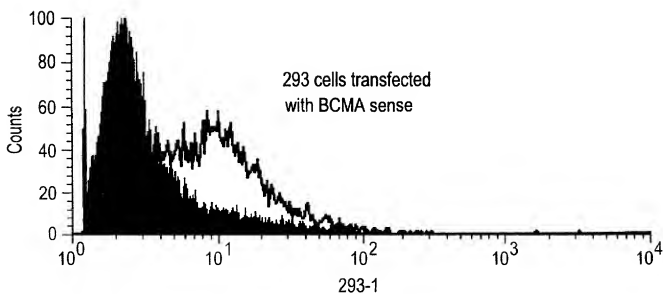


FIG. 15A

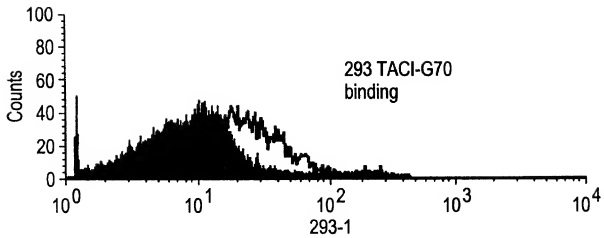


FIG. 15B

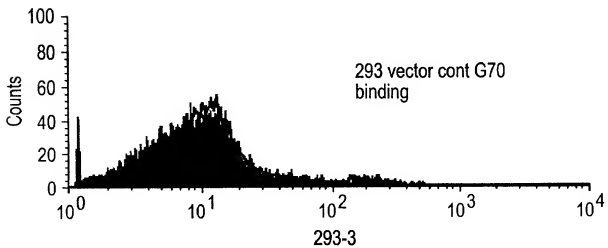


FIG. 16A

FIG. 16A

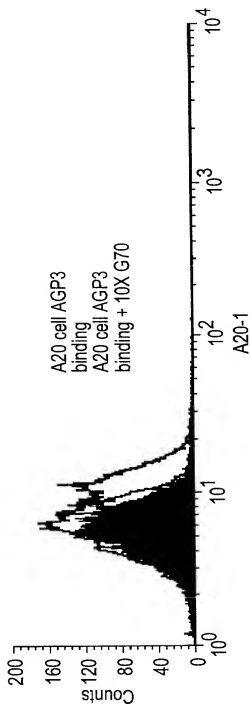


FIG. 16B

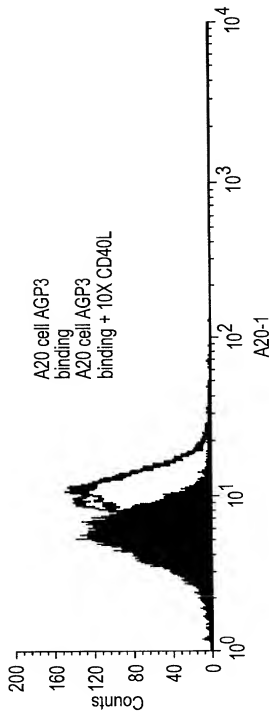


FIG. 16C

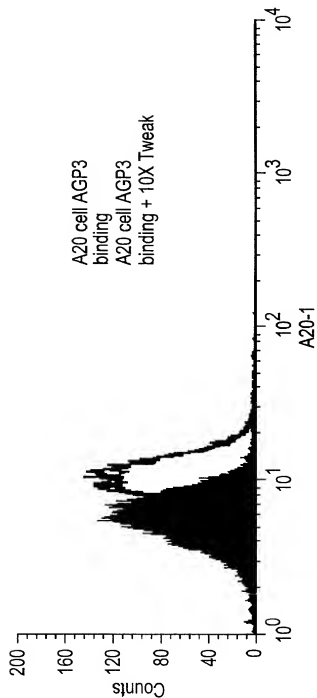


FIG. 16C

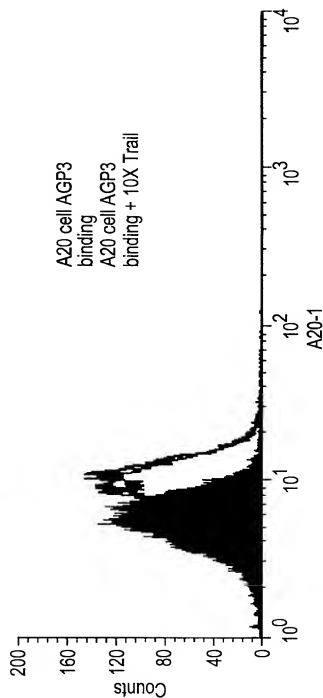


FIG. 16D

FIG. 17A

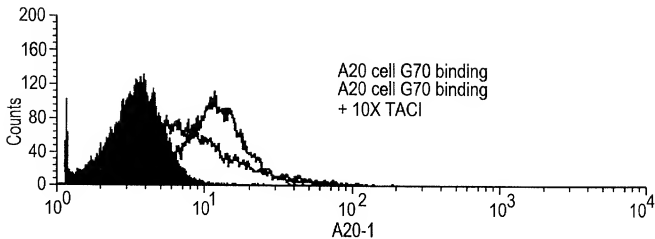


FIG. 17B

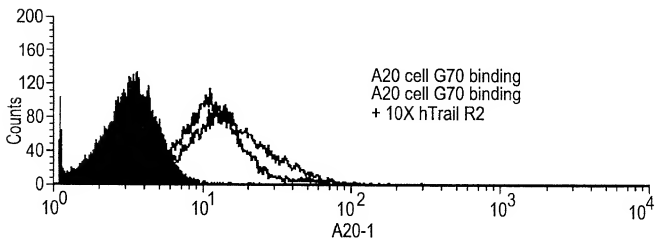


FIG. 17C

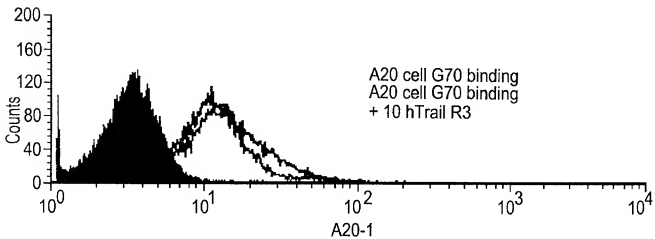


FIG. 18

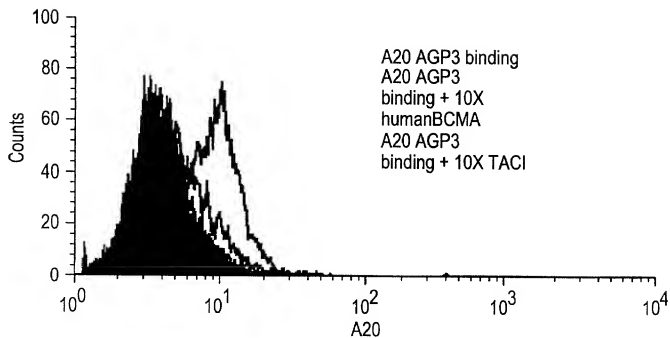


FIG. 19A

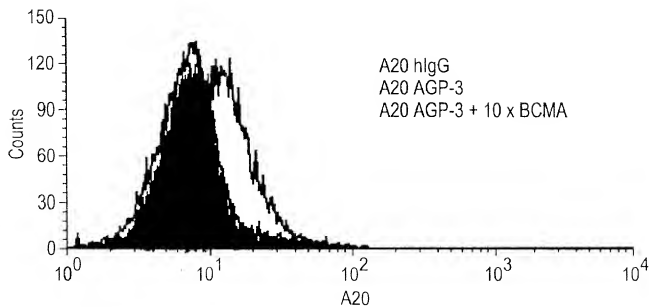


FIG. 19B

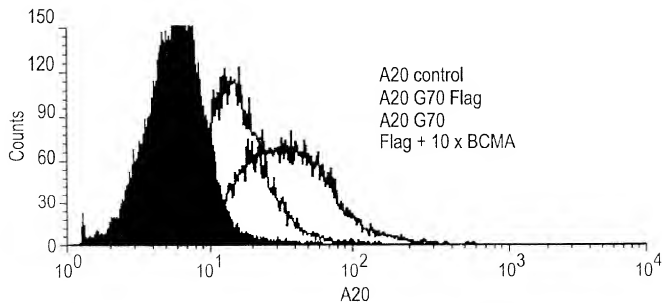


FIG. 20A

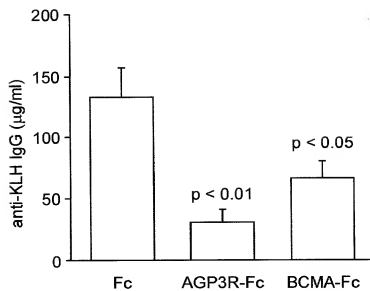


FIG. 20B

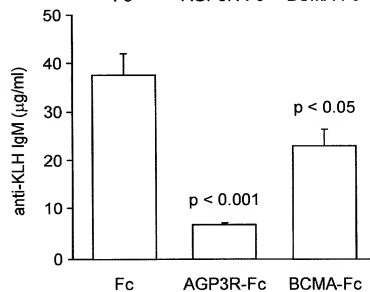


FIG. 20C

